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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/015,822	12/10/2001	Kevin P. Baker	GNE.2830P1C38	8184

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EXAMINER	
BUNNER, BRIDGET E	

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 11/04/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/015,822	BAKER ET AL.	
	Examiner	Art Unit	
	Bridget E. Bunner	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *06 March 2003*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *28-40* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *28-40* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *10 December 2001* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *8/16/02; 11/8/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Status of Application, Amendments and/or Claims

The amendments of 10 December 2001 and 10 June 2002 have been entered in full. Claims 1-27 are cancelled and claims 28-40 are added.

Claims 28-40 are under consideration in the instant application.

Information Disclosure Statement

The information disclosure statements (IDS) submitted on 16 September 2002 and 08 November 2002 have been considered by the examiner. However, since the Blast results cited therein are not true publications with a publication date, they are not fully in compliance with 37 CFR 1.97 and thus they will not be printed on the face of the patent issuing from this application.

Priority

Applicant's claim for priority under 35 U.S.C. 120 and 119(e) is acknowledged. The polynucleotide of SEQ ID NO: 373 and the polypeptide of SEQ ID NO: 374 of the instant application are fully disclosed in the prior applications of 60/108,867 (11/17/1998), PCT/US99/20111 (9/1/1999), 09/403,297 (10/18/1999), PCT/US00/03565 (2/11/2000), PCT/US00/04342 (2/18/2000), and 09/946,374 (9/4/2001).

Specification

1. The disclosure is objected to because of the following informalities:

2. The disclosure is objected to because it contains numerous embedded hyperlinks and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlinks and/or other form of browser-executable code. See MPEP § 608.01.

3. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

The following title is suggested: "TRANSMEMBRANE POLYPEPTIDE".

Appropriate correction is required.

Claim Rejections - 35 USC § 101 and 35 USC § 112

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 28-40 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a credible, specific and substantial asserted utility or a well established utility. Novel biological molecules lack well established utility and must undergo extensive experimentation.

Specifically, claims 28-40 are directed to an isolated polypeptide having at least 80%, 85%, 90%, 95%, and 99% amino acid sequence identity to (a) the amino acid sequence of the polypeptide shown in Figure 218 (SEQ ID NO: 374), (b) the amino acid sequence of the polypeptide shown in Figure 218 (SEQ ID NO: 374) lacking its associated signal peptide, (c) the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 218 (SEQ ID NO: 374), (d) the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 218 (SEQ ID NO: 374) lacking its associated signal peptide, or (e) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited

under ATCC accession number 203465. The claims are also directed to an isolated polypeptide comprising the previously mentioned subparts (a), (b), (c), (d), or (e). The claims recite a chimeric polypeptide comprising a polypeptide fused to a heterologous polypeptide.

The specification discloses that "many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel transmembrane proteins. We herein describe the identification and characterization of a novel transmembrane protein designated herein as PRO1759" (pg 32, lines 16-20) However, the instant specification does not teach any significance or functional characteristics of the PRO1759 polynucleotide (SEQ ID NO: 373) or polypeptide (SEQ ID NO: 374). The specification also does not disclose any methods or working examples that indicate the polynucleotides and polypeptide of the instant invention are involved in any activity. There is no biological activity, expression pattern, phenotype, disease or condition, ligand, binding partner, or any other specific feature that is disclosed as being associated with PRO1759. Without any information as to the specific properties of PRO1759, the mere identification of such as being a transmembrane polypeptide is not sufficient to impart any particular utility to the claimed polypeptides. Since significant further research would be required of the skilled artisan to determine how the claimed polynucleotide and polypeptide are involved in any activities, the asserted utilities are not substantial. Since the utility is not presented in mature form and significant further research is required, the utility is not substantial. The specification asserts the following as patentable utilities for the claimed putative polypeptide (SEQ ID NO: 374):

1) to produce a variant polypeptide (pg 365, lines 16-38 through pg 366, lines 1-13)

2) to screen for peptides/ligands/small molecules which specifically bind the polypeptide (pg 381-383)

3) in tissue typing (pg 379, lines 24-26)

4) to produce antibodies against the polypeptide (pg 384, lines 7-38 through pg 388)

5) as a therapeutic agent (pg 379, lines 28-38 through pg 380)

Each of these shall be addressed in turn.

1) to produce a variant polypeptide. This asserted utility is not specific or substantial. Such assays can be performed with any polypeptide. Further, the specification discloses nothing specific or substantial for the variant polypeptide that is produced by this method. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

2) to screen for peptides/ligands/small molecules which specifically bind the polypeptide. This asserted utility is not specific or substantial. Such assays can be performed with any polypeptide. Additionally, the specification discloses nothing specific or substantial for the agents that can be identified by this method. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

3) in tissue typing. This asserted utility is not specific or substantial. Such assays can be performed with any polypeptide. Further, the specification does not disclose specific amino acid sequences for use as markers. The specification also does not disclose the tissue(s) that PRO1759 is normally or abnormally present in. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

4) to produce antibodies against the polypeptide. This asserted utility is not specific or substantial. Antibodies can be made to any polypeptide. However, if the specification discloses nothing specific and substantial about the polypeptide, therefore both polypeptide and its antibodies have no patentable utility.

5) as a therapeutic agent. This asserted utility is not specific or substantial. The specification does not disclose which cells or tissues are to be targeted or which diseases or diseases are to be treated. The specification does not disclose if the cells, tissues, or disorders are associated with altered levels or forms of the PRO1759 polypeptide. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

Additionally, at pages 517-519 of the specification, it is disclosed that nucleic acids encoding PRO1759 had a ΔCt value of at least 1.0 for one primary lung tumor (HF-000840), one primary colon tumor (HF-000795), and HF-001296 but not for all tested colon or lung primary tumors or cultured cell lines. At page 510, ΔCt is defined as one unit corresponds to 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold amplification, and so on. At pg 513, lines 9-12, ΔCt is defined as the threshold PCR cycle, or the cycle at which the reporter signal accumulates above the background level of fluorescence. The specification further indicates that ΔCt is used as "a quantitative measurement of the relative number of starting copies of a particular target sequence in a nucleic acid sample when comparing cancer DNA results to normal human DNA results." The Examiner is unable to find, either in the specification or in the art, an explanation of how ΔCt values are calculated, nor what

the significance of such are. It is noted that at page 516, lines 30-31, it is stated that samples are used if their values are within 1 Ct of the 'normal standard'. It is further noted that the ΔCt values at pages 517-523 are (a) expressed with values to one one-hundredth of a unit (e.g. 1.32), and (b) varied from a little over 1 to over 4 in some instances. It is not clear how measurements of hundredths of a PCR cycle can be made, nor what the significance of a difference of 1 or 2 or 4 PCR cycles would be. Given the paucity of information, the data do not support the implicit conclusion of the specification that PRO1759 shows a positive correlation with lung cancer or colon cancer, much less that the levels of PRO1759 would be diagnostic of such. Even *if* the data demonstrated a slight increase in copy number of PRO1759 nucleic acids in primary tumors, such would not be indicative of a use of the encoded polypeptide as a diagnostic agent. Cancerous tissue is known to be aneuploid, that is, having an abnormal number of chromosomes (see Sen, 2000, Curr. Opin. Oncol. 12:82-88). The data presented in the specification were not corrected for aneuploidy. A slight amplification of a gene does not necessarily mean overexpression in a cancer tissue, but can merely be an indication that the cancer tissue is aneuploid. The preliminary data were not supported by analysis of mRNA or protein expression, for example. Also, the literature reports that it does not necessarily follow that an increase in gene copy number results in increased gene expression and increased polypeptide expression, such that the claimed polypeptides would be useful for diagnosis of cancer or as a drug target. For example, Pennica et al. (1998, PNAS USA 95:14717-14722) disclose that:

> "An analysis of *WISP*-1 gene amplification and expression in human colon tumors showed a correlation between DNA amplification and overexpression, whereas overexpression of *WISP*-3 RNA was seen in the absence of DNA amplification. In contrast, *WISP*-2 DNA was amplified in the colon tumors, but its mRNA expression was significantly reduced in the majority of

> tumors compared with the expression in normal colonic mucosa from the same patient."

See pg 14722, second paragraph of left column; pg 14720-14721, "Amplification and Aberrant Expression of *WISPs* in Human Colon Tumors." Finally, even if gene amplification correlates with increased transcription, it does not always follow that protein levels are also amplified. See Haynes et al. (Electrophoresis 19:1862-1871, 1998), who studied more than 80 proteins relatively homogeneous in half-life and expression level, and found no strong correlation between protein and transcript level. For some genes, equivalent mRNA levels translated into protein abundances which varied more than 50-fold. Haynes et al. concluded that the protein levels cannot be accurately predicted from the level of the corresponding mRNA transcript (p. 1863, second paragraph, and Figure 1). Therefore, data pertaining to PRO1759 nucleic acids do not necessarily indicate anything significant regarding the claimed PRO1759 polypeptides. Thus, the data do not support the implicit assertion that PRO1759 can be used as a cancer diagnostic and the art indicates that it is not the norm that gene amplification, or even increased transcription, results in increased protein levels. Significant further research would have been required of the skilled artisan to determine whether PRO1759 is overexpressed in any cancer to the extent that it could be used as a cancer diagnostic, and thus the implicitly asserted utility is not substantial.

5. Claims 28-40 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

5a. However, even if the claimed invention is eventually deemed to have a credible, specific and substantial asserted utility or a well established utility, claims 28-33, 36-37, and 39-40 would remain rejected under 35 U.S.C. § 112, first paragraph. Specifically, the specification teaches that the term "'PRO/number polypeptide' and 'PRO/number' wherein the term 'number' is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (pg 31, lines 1-6). The PRO1759 nucleic acids and polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods (pg 311, lines 6-8). The specification discloses that a PRO polypeptide variant is defined as an active PRO polypeptide having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence, a full-length native sequence PRO polypeptide sequence lacking the signal peptide, an extracellular domain of a PRO polypeptide, with or without signal peptide, or any other fragment of a full-length PRO polypeptide sequence (pg 312, lines 5-33). However, the specification does not teach any variant, fragment, or derivative of the PRO1759 polypeptide other than the full-length amino acid sequence of SEQ ID NO: 374. The specification also does not teach functional or structural characteristics of the polypeptide variants, fragments, and derivatives (including the extracellular domain) recited in the claims.

The problem of predicting protein and DNA structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein and DNA is extremely complex. While it is known that many amino acid substitutions are generally possible in any given protein the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions

in the sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. These or other regions may also be critical determinants of antigenicity. These regions can tolerate only relatively conservative substitutions or no substitutions (see Wells, 1990, Biochemistry 29:8509-8517; Ngo et al., 1994, The Protein Folding Problem and Tertiary Structure Prediction, pp. 492-495). However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the DNA and protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions. Even if an active or binding site were identified in the specification, they may not be sufficient, as the ordinary artisan would immediately recognize that an active or binding site must assume the proper three-dimensional configuration to be active, which conformation is dependent upon surrounding residues; therefore substitution of non-essential residues can often destroy activity. The art recognizes that function cannot be predicted from structure alone (Bork, 2000, Genome Research 10:398-400; Skolnick et al., 2000, Trends in Biotech. 18(1):34-39, especially p. 36 at Box 2; Doerks et al., 1998, Trends in Genetics 14:248-250; Smith et al., 1997, Nature Biotechnology 15:1222-1223; Brenner, 1999, Trends in Genetics 15:132-133; Bork et al., 1996, Trends in Genetics 12:425-427).

Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required

in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function, and the breadth of the claims which fail to recite any structural or functional limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

6. Claims 28-33, 36-37, and 39-40 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are directed to an isolated polypeptide having at least 80%, 85%, 90%, 95%, and 99% amino acid sequence identity to (a) the amino acid sequence of the polypeptide shown in Figure 219 (SEQ ID NO: 374), (b) the amino acid sequence of the polypeptide shown in Figure 219 (SEQ ID NO: 374) lacking its associated signal peptide, (c) the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 219 (SEQ ID NO: 374), (d) the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 219 (SEQ ID NO: 374) lacking its associated signal peptide, or (e) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 203465. The claims are also directed to an isolated polypeptide comprising the previously mentioned subparts (a), (b), (c), (d), or (e). The claims recite a chimeric polypeptide comprising a polypeptide fused to a heterologous polypeptide. The claims do not require that the polypeptide possess any particular biological activity, nor any particular

conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus. Additionally, the description of one polynucleotide species (SEQ ID NO: 373) and one polypeptide species (SEQ ID NO: 374) is not adequate written description of an entire genus of functionally equivalent polynucleotides and polypeptides which incorporate all variants and fragments and with at least 80%, 85%, 90%, 95%, and 99% sequence identity to the polypeptide comprising the amino acid sequence of SEQ ID NO: 374.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention.* The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed"* (See page 1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed" (See *Vas-Cath* at page 1116).

With the exception of the sequences referred to above, the skilled artisan cannot envision the detailed chemical structure of the encompassed polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The polypeptide itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only an isolated polypeptide consisting of the amino acid sequence of SEQ ID NO: 374, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

35 U.S.C. § 112, Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

7. Claims 28-33, 36-37, and 39-40 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

8. The polypeptide identified as PRO1759 is disclosed as having multiple transmembrane domains (see for example, Figure 218), which would result in multiple extracellular domains. Therefore, it is unclear what is meant by the recitation of "**the** extracellular domain" in claims 28-33, 36-37, and 39-40. Further, if the polypeptide had an extracellular domain, the recitation of "the extracellular domain"..."lacking its associated signal sequence" (claim 28, part (d), for example) is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell.

Conclusion

No claims are allowable.

The art made of record and not relied upon is considered pertinent to applicant's disclosure:

LaFleur et al. U.S. Patent 6,569,992 (teaches SEQ ID NO: 374 of the instant application, but did not disclose until 8/5/1999; see patent SEQ ID NOs: 97 and 167, for example. The instant application fully discloses SEQ ID NO: 374 in the provisional application of 60/108,867 filed 11/17/1998)

Clark et al. Genome Res 13(10) : 2265-2270, 2003 (review discussing the SDPI project).

Strausberg et al. Proc Natl Acad Sci USA 99(26): 16899-16903, 2002 (review of project to identify human and mouse genes).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Bridget E. Bunner whose telephone number is (571) 272-0881. The examiner can normally be reached on 8:30-4:30 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Brenda Brumback can be reached on (571) 272-0961. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

BEB
Art Unit 1647
12 October 2004

Bridget E. Bunner